

## SEQUENCE LISTING

<110> HuBit Genomix, Inc.  
Doi, Toshio

<120> A method for detecting diabetic nephropathy and kits therefor, agents for preventing and/or treating diabetic nephropathy, a method for identifying substances effective in prevention and/or treatment and kits therefor

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<150> JP P2003-319538

<151> 2003-09-11

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<170> PatentIn Ver. 2.1

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tgc cat ggg gac tgc ccc ttt cca ctg gct gac cac ctc aac tca acc Cys His Gly Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr 340 345 350	1533
aac cat gcc att gtg cag acc ctg gtc aat tct gtc aat tcc agt atc Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile 355 360 365	1581
ccc aaa gcc tgt tgt gtg ccc act gaa ctg agt gcc atc tcc atg ctg Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu 370 375 380	1629

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 385 390 395 400

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 Val Val Glu Gly Cys Gly Cys Arg  
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aaaaaaaaat ggaaaaaatc cctaaacatt caccttgacc ttatttatga ctttacgtgc 1904

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<220>

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<223> Description of Artificial Sequence: synthetic DNA

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25

<210> 14

<211> 27

<212> DNA

<213> Mus musculus

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27

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<223> Description of Artificial Sequence: synthetic DNA

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19

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&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: synthetic DNA

&lt;400&gt; 16

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18

&lt;210&gt; 17

&lt;211&gt; 262

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: synthetic DNA

&lt;400&gt; 17

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aaaatgtgca ctattcgat gagcttcgtg aagggttggg gagccgaata ccaccggcag 180
gatgttacca gcacccctg ctggattgag atccatctgc atggccctct ccagtggctg 240
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&lt;210&gt; 18

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

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25

&lt;210&gt; 19

&lt;211&gt; 4978

&lt;212&gt; mRNA

&lt;213&gt; Homo sapiens



&lt;220&gt;

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&lt;222&gt; (241).. (2553)

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ccctcggctc ggagaggccc ttcggcctga gggagcctcg ccgcccgtcc ccggcacacg 180
cgcagccccg gcctctcggc ctctgccgga gaaacagtig ggaccctga ttttagcagg 240

atg gcc caa tgg aat cag cta cag cag ctt gac aca cgg tac ctg gag 288
Met Ala Gln Trp Asn Gln Leu Gln Gln Leu Asp Thr Arg Tyr Leu Glu
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cag ctc cat cag ctc tac agt gac agc ttc cca atg gag ctg cgg cag 336
Gln Leu His Gln Leu Tyr Ser Asp Ser Phe Pro Met Glu Leu Arg Gln
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ttt ctg gcc cct tgg att gag agt caa gat tgg gca tat gcg gcc agc 384
Phe Leu Ala Pro Trp Ile Glu Ser Gln Asp Trp Ala Tyr Ala Ala Ser
  35           40           45

aaa gaa tca cat gcc act ttg gtg ttt cat aat ctc ctg gga gag att 432
Lys Glu Ser His Ala Thr Leu Val Phe His Asn Leu Leu Gly Glu Ile
  50           55           60

gac cag cag tat agc cgc ttc ctg caa gag tgc aat gtt ctc tat cag 480
Asp Gln Gln Tyr Ser Arg Phe Leu Gln Glu Ser Asn Val Leu Tyr Gln
  65           70           75           80

cac aat cta cga aga atc aag cag ttt ctt cag agc agg tat ctt gag 528
His Asn Leu Arg Arg Ile Lys Gln Phe Leu Gln Ser Arg Tyr Leu Glu
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aag cca atg gag att gcc cgg att gtg gcc cgg tgc ctg tgg gaa gaa 576
Lys Pro Met Glu Ile Ala Arg Ile Val Ala Arg Cys Leu Trp Glu Glu
 100           105           110

tca cgc ctt cta cag act gca gcc act gcg gcc cag caa ggg ggc cag 624
Ser Arg Leu Leu Gln Thr Ala Ala Thr Ala Ala Gln Gln Gly Gly Gln
 115           120           125

gcc aac cac ccc aca gca gcc gtg gtg acg gag aag cag cag atg ctg 672
Ala Asn His Pro Thr Ala Ala Val Val Thr Glu Lys Gln Gln Met Leu
 130           135           140

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aaa acc ctc aag agt caa gga gac atg caa gat ctg aat gga aac aac Lys Thr Leu Lys Ser Gln Gly Asp Met Gln Asp Leu Asn Gly Asn Asn 180 185 190	816
cag tca gtg acc agg cag aag atg cag cag ctg gaa cag atg ctc act Gln Ser Val Thr Arg Gln Lys Met Gln Gln Leu Glu Gln Met Leu Thr 195 200 205	864
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caa aaa gtt tcc tac aaa ggg gac ccc att gta cag cac cgg ccg atg Gln Lys Val Ser Tyr Lys Gly Asp Pro Ile Val Gln His Arg Pro Met 290 295 300	1152
ctg gag gag aga atc gtg gag ctg ttt aga aac tta atg aaa agt gcc Leu Glu Glu Arg Ile Val Glu Leu Phe Arg Asn Leu Met Lys Ser Ala 305 310 315 320	1200
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Thr Leu Ala Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln Cys			
95	100	105 110	
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Lys Asp Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys Arg			
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Ile Gly Pro Phe Phe Asp Gly Ser Ile Arg Trp Leu Val Leu Leu Ile			
145	150	155	
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Ser Met Ala Val Cys Ile Ile Ala Met Ile Ile Phe Ser Ser Cys Phe			
160	165	170	
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Cys Tyr Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Arg Arg Tyr Asn			
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Lys Asp Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu			
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Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Arg			
225	230	235	
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Gln Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg			
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Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser			



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Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu				
275	280	285		
aac ata ctt ggt ttc ata gcg gca gac att aaa ggt aca ggt tcc tgg	1454			
Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp				
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act cag ctc tat ttg att act gat tac cat gaa aat gga tct ctc tat	1502			
Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr				
305	310	315		
gac ttc ctg aaa tgt gct aca ctg gac acc aga gcc ctg ctt aaa ttg	1550			
Asp Phe Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys Leu				
320	325	330		
gct tat tca gct gcc tgt ggt ctg tgc cac ctg cac aca gaa att tat	1598			
Ala Tyr Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile Tyr				
335	340	345	350	
ggc acc caa gga aag ccc gca att gct cat cga gac cta aag agc aaa	1646			
Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys				
355	360	365		
aac atc ctc atc aag aaa aat ggg agt tgc tgc att gct gac ctg ggc	1694			
Asn Ile Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu Gly				
370	375	380		
ctt gct gtt aaa ttc aac agt gac aca aat gaa gtt gat gtg ccc ttg	1742			
Leu Ala Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Val Pro Leu				
385	390	395		
aat acc agg gtg ggc acc aaa cgc tac atg gct ccc gaa gtg ctg gac	1790			
Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp				
400	405	410		
gaa agc ctg aac aaa aac cac ttc cag ccc tac atc atg gct gac atc	1838			
Glu Ser Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp Ile				
415	420	425	430	
tac agc ttc ggc cta atc att tgg gag atg gct cgt cgt tgt atc aca	1886			
Tyr Ser Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile Thr				
435	440	445		
gga ggg atc gtg gaa gaa tac caa ttg cca tat tac aac atg gta ccg	1934			
Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val Pro				

450	455	460	
agt gat ccg tca tac gaa gat atg cgt gag gtt gtg tgt gtc aaa cgt			1982
Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys Arg			
465	470	475	
ttg cgg cca att gtg tct aat cgg tgg aac agt gat gaa tgt cta cga			2030
Leu Arg Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu Arg			
480	485	490	
gca gtt ttg aag cta atg tca gaa tgc tgg gcc cac aat cca gcc tcc			2078
Ala Val Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala Ser			
495	500	505	510
aga ctc aca gca ttg aga att aag aag acg ctt gcc aag atg gtt gaa			2126
Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val Glu			
515	520	525	
tcc caa gat gta aaa atc tga tggtaaacc atcggaggag aaactctaga			2177
Ser Gln Asp Val Lys Ile			
530			
ctgcaagaac tgtttttacc catggcatgg gtggaattag agtggataa ggatgttaac			2237
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19

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<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic DNA

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20

<210> 23  
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19

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21